Amendments to the Claims:

The listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (original): A method of screening for an agent that modulates the differentiation into osteoblasts, comprising: (a) preparing a first gene or gene family expression profile of a cell population comprising MC3T3-E1 or MC3T3-1b cells and/or assaying an activity of a protein encoded by at least one gene or a member of a gene family of Table 1 of a cell population comprising MC3T3-E1 or MC3T3-1b cells; (b) exposing the cell population to the agent; (c) preparing second gene or gene family expression profile of the agent exposed cell population and/or assaying an activity of a protein encoded by at least one gene or a member of a gene family of Table 1 of the exposed cell population; and (d) comparing the first and second expression profiles or first and second activities to an expression profile and/or an activity of an osteblastic differentiated MC3T3-E1 or MC3T3-1b cell population.

Claim 2 (original): The method of claim 1, wherein the gene expression profiles comprise the expression levels for a set of genes that are differentially regulated in MC3T3-E1 or MC3T3-1b cells compared to an osteblastic differentiated MC3T3-E1 or MC3T3-1b cell population.

Claim 3 (original): The method of claim 1, wherein the agent modulates the level of expression or activity for at least one gene in the MC3T3-E1 or MC3T3-1b cell population to the expression level found in an osteblastic differentiated MC3T3-E1 or MC3T3-1b cell population.

Claim 4 (original): The method of claim 1, wherein the gene expression profiles or activity level comprise the expression or activity levels in a cell of at least two genes or members of a gene family in Table 1.

Claim 5 (original): The method of claim 1, wherein the gene is Hey1.

Claim 6 (original): A method of diagnosing a condition characterized by abnormal deposition of bone tissue, comprising detecting in a tissue sample the level of expression of and/or activity of a protein encoded by at least one gene or member of a gene family of Table 1, wherein differential expression or activity of the gene or member of a gene family is indicative of abnormal bone tissue deposition.

Claim 7 (original): A method of monitoring the treatment of a patient with a condition characterized by abnormal bone tissue deposition, comprising: (a) administering a pharmaceutical composition to the patient; (b) preparing a gene expression profile from a cell or tissue sample from the patient and/or assaying an activity of a protein encoded by at least one gene or a member of a gene family of Table 1; and (c) comparing the patient expression profile or activity to an expression profile or activity from a MC3T3-E1 or MC3T3-1b cell population or an osteblastic differentiated MC3T3-E1 or MC3T3-1b cell population.

Claim 8 (original): A method of diagnosing a condition characterized by an abnormal rate of formation of osteoblasts, comprising detecting in a tissue sample a level of expression of and/or activity of a protein encoded by at least one gene or member of a gene family from Table 1, wherein differential expression and/or activity of the gene or member of a gene family is indicative of an abnormal rate of formation of osteoblasts.

Claim 9 (original): A method of monitoring the treatment of a patient with a condition characterized by abnormal rate of formation of osteoblasts, comprising: (a) administering a pharmaceutical composition to the patient; (b) preparing a gene expression profile and/or assaying an activity of at least one gene or member of a gene family from Table 1 in a cell or tissue sample from the patient; and (c) comparing the patient gene expression profile and/or activity to a gene expression profile or activity from a MC3T3-E1 or MC3T3-1b cell population or an osteblastic differentiated MC3T3-E1 or MC3T3-1b cell population.

Claim 10 (original): A method of diagnosing osteoporosis in a patient, comprising detecting the level of expression and/or activity in a tissue sample of at least one gene or member of a gene family from Table 1; wherein differential expression or activity is indicative of osteoporosis.

Claim 11 (original): A method of monitoring the treatment of a patient with osteoporosis, comprising: (a) administering a pharmaceutical composition to the patient; (b) preparing a gene expression profile and/or assaying an activity of at least one gene or member of a gene family of Table 1 in a cell or tissue sample from the patient; and (c) comparing the patient gene expression profile and/or activity to a gene expression profile or activity in a MC3T3-E1 or MC3T3-1b cell population and/or an osteblastic differentiated MC3T3-E1 or MC3T3-1b cell population.

Claim 12 (original): A method of screening for an agent capable of ameliorating the effects of osteoporosis, comprising: (a) exposing a cell to the agent; and (b) detecting the expression and/or activity level of one or more genes or members of a gene family of Table 1.

Claim 13 (original): A method of monitoring the progression of bone tissue deposition in a patient, comprising detecting the level of expression and/or activity in a tissue sample of at least one gene or member of a gene family from Table 1; wherein differential expression and/or activity is indicative of bone tissue deposition.

Claim 14 (original): A method of screening for an agent capable of modulating the deposition of bone tissue, comprising: (a) exposing a cell to the agent; and (b) detecting the expression and/or activity level of at least one gene or member of a gene family of Table 1.

Claim 15 (currently amended): The method of ~~any one of claims 1-14~~ claim 1, wherein expression and/or activity levels of at least 2 genes are detected.

Claim 16 (currently amended): The method of ~~any one of claims 1-14~~ claim 1, wherein expression and/or activity levels of at least 3 genes are detected.

Claim 17 (currently amended): The method of ~~any one of claims 1-15~~ claim 1, wherein expression and/or activity levels of at least 4, 5, 6, 7, 8, 9, 10 or 11 genes are detected.

Claim 18 (currently amended): The method of ~~any one of claims 1-14~~ claim 1, wherein expression and/or activity levels of all the genes in Table 1 are detected.

Claim 19 (currently amended): The method of ~~any one of claims 1-14~~ claim 1, wherein expression and/or activity levels of all the genes in Table 2 are detected.

Claim 20 (currently amended): The method of ~~any one of claims 1-14~~ claim 1, wherein expression and/or activity levels of all the genes in Table 3 are detected.

Claim 21 (original): A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.

Claim 22 (original): The composition according to claim 21, wherein the composition comprises at least 3 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.

Claim 23 (original): The composition according to claim 21, wherein the composition comprises at least 5 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.

Claim 24 (original): The composition according to claim 21, wherein the composition comprises at least 7 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.

Claim 25 (original): The composition according to claim 21, wherein the composition comprises at least 10 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.

Claim 26 (currently amended): The composition according to ~~any one of claims 21-25~~ claim 21, wherein the oligonucleotides are attached to a solid support.

Claim 27 (currently amended): The composition according to claim ~~25~~ 26, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material and a silicon support.

Claim 28 (original): A solid support to which is attached at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.

Claim 29 (original): The solid support according to claim 28, wherein at least one oligonucleotide is attached covalently.

Claim 30 (original): The solid support according to claim 28, wherein at least one oligonucleotide is attached non-covalently.

Claim 31 (original): The solid support of claim 28, wherein the solid support is an array comprising at least 10 different oligonucleotides in discrete locations per square centimeter.

Claim 32 (original): The solid support of claim 28, wherein the array comprises at least 100 different oligonucleotides in discrete locations per square centimeter.

Claim 33 (original): The solid support of claim 28, wherein the array comprises at least 1000 different oligonucleotides in discrete locations per square centimeter.

Claim 34 (original): The solid support of claim 28, wherein the array comprises at least 10000 different oligonucleotides in discrete locations per square centimeter.

Claim 35 (original): A computer system comprising: (a) a database containing information identifying the expression and /or activity level in osteoblasts of a set of genes comprising one or more genes or members of a gene family in Table 1; and (b) a user interface to view the information.

Claim 36 (original): The computer system of claim 35, wherein the database further comprises sequence information for the genes or gene families.

Claim 37 (original): The computer system of claim 35, wherein the database further comprises information identifying the expression and/or activity level in MC3T3-E1 and/or MC3T3-1b cells of at least one gene or member of a gene family of Table 1.

Claim 38 (original): The computer system of claim 35, wherein the database further comprises information identifying the expression level a set of genes indicative of a condition characterized by abnormal bone tissue deposition.

Claim 39 (currently amended): The computer system of ~~any of claims 35-38~~ claim 35, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

Claim 40 (original): The computer system of claim 39, wherein the external database is GenBank.

Claim 41 (currently amended): The method of using a computer system of ~~any one of claims 35-40~~ claim 35 to present information identifying the expression level in a tissue or cell of a set of genes comprising at least two of the genes or members of gene families in Table 1, comprising: (a) comparing the expression level of at least one gene or member of a gene family in Table 1 in the tissue or cell to the level of expression of the gene in the database.

Claim 42 (original): The method of claim 41, wherein the expression levels of at least two genes are compared.

Claim 43 (original): The method of claim 41, wherein the expression levels of at least five genes are compared.

Claim 44 (original): The method of claim 41, wherein the expression levels of at least ten genes are compared.

Claim 45 (original): The method of claim 41, further comprising the step of displaying the level of expression of at lest one gene in the tissue or cell sample compared to the expression level in osteblastic differentiated MC3T3-E1 cells and/or MC3T3-1b cells.

Claim 46 (new): The method of claim 5, wherein expression and/or activity levels of at least 2 genes are detected.

Claim 47 (new): The method of claim 5, wherein expression and/or activity levels of at least 3 genes are detected.

Claim 48 (new): The method of claim 5, wherein expression and/or activity levels of at least 4, 5, 6, 7, 8, 9, 10 or 11 genes are detected.

Claim 49 (new): The method of claim 5, wherein expression and/or activity levels of all the genes in Table 1 are detected.

Claim 50 (new): The method of claim 5, wherein expression and/or activity levels of all the genes in Table 2 are detected.

Claim 51 (new): The method of claim 5, wherein expression and/or activity levels of all the genes in Table 3 are detected.